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**Association of Elevated Urinary  
miR-126, miR-155 and miR-29b with Diabetic Kidney Disease**

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1   **ABSTRACT**

2   Effective diabetic kidney disease (DKD) biomarkers remain elusive, and urinary  
3   microRNAs (miRNAs) represent a potential source of novel non-invasive disease  
4   sentinels. We profiled 754 miRNAs in pooled urine samples from DKD patients (n = 20),  
5   detecting significantly increased miR-126, miR-155 and miR-29b compared to controls  
6   (n = 20). These results were confirmed in an independent cohort of 89 DKD patients,  
7   62 diabetic patients without DKD and 41 controls: miR-126 (2.8-fold increase;  
8   p<0.0001), miR-155 (1.8-fold; p<0.001) and miR-29b (4.6-fold; p = 0.024). Combined  
9   receiver operating characteristic curve analysis resulted in an area under the curve of  
10   0.8. A relative quantification threshold equivalent to 80% sensitivity for each miRNA  
11   gave a positive signal for 48% of DKD patients compared to 3.6% of diabetic patients  
12   without DKD. Laser capture microdissection of renal biopsies followed by RT-qPCR  
13   detected miR-155 in glomeruli, proximal and distal tubules, while miR-126 and miR-  
14   29b were most abundant in glomerular extracts. Subsequent experiments showed  
15   miR-126 and miR-29b enrichment in glomerular endothelial cells (GEnCs) compared to  
16   podocytes, proximal tubular epithelial cells and fibroblasts. Significantly increased miR-  
17   126 and miR-29b were detected in GEnC conditioned medium in response to tumour  
18   necrosis factor-alpha and transforming growth factor-beta 1, respectively. Our data  
19   reveal an altered urinary miRNA profile associated with DKD and link these variations  
20   to miRNA release from GEnCs.

21

22   **Keywords:** microRNAs, urine, biomarker, diabetic kidney disease, chronic kidney  
23   disease

24

25    **Abbreviations:**

26    ACR            albumin:creatinine ratio

27    CKD            chronic kidney disease

28    DKD            diabetic kidney disease

29    eGFR            estimated glomerular filtration rate

30    GEnC            glomerular endothelial cell

31    KDIGO           kidney disease: improving global outcomes

32    NKF KDOQI    National Kidney Foundation kidney disease outcomes quality initiative

33    LCM            laser capture microdissection

34    MDRD           modification of diet in renal disease

35    miRNA           microRNA

36    PTC            proximal tubular epithelial cell

37    RIISC            renal impairment in secondary care study

38

39

## 40    **Introduction**

41    Recent estimates suggest that 1 in 12 of the global population suffers from diabetes  
42    mellitus, approximately 40 % of those affected will go on to develop diabetic kidney  
43    disease (DKD).<sup>1</sup> DKD is the leading cause of end-stage renal disease and predisposing  
44    factors include genetic causes, ethnicity, hyperglycaemia, insulin resistance,  
45    intraglomerular hypertension and hyperfiltration.<sup>2,3</sup>

46            Hyperglycaemia results in numerous deleterious consequences including  
47    upregulated cytokine synthesis, renin-angiotensin system activation, generation of  
48    advanced glycation end products and reactive oxygen species, and increased protein  
49    kinase C activity.<sup>4,5</sup> Nitric oxide and NF-κB pathway-driven loss of endothelial and  
50    vascular modulation have been implicated in insulin resistance, and early DKD may  
51    be associated with insulin signaling defects specific to the podocyte.<sup>6</sup> These insults  
52    result in loss of glomerular filtration rate and ultimately to renal failure from  
53    mesangial hyperexpansion, nodular glomerulosclerosis and tubulointerstitial  
54    fibrosis.<sup>7</sup>

55            Detection of urinary microalbuminuria currently forms the basis of DKD  
56    progression monitoring, varying from normal mean albuminuria values around 10  
57    mg/day to a diagnosis of microalbuminuria at 30–300 mg/day and macroalbuminuria  
58    above 300 mg/day.<sup>8</sup> Prognosis is complicated, since not all microalbuminuric  
59    patients progress to overt nephropathy. A number of novel biomarkers have been  
60    assessed for utility in DKD but none are being used as routine clinical markers, and  
61    they may lack specificity and sensitivity to predict individual DKD patient outcomes.  
62    In light of the above, novel markers that can discriminate aetiology, progression  
63    and/or response to treatment remain highly desirable.

MicroRNAs (miRNAs) are ubiquitously-expressed short noncoding RNAs that regulate the expression of most protein coding genes in the human genome, and detection of miR-192, miR-194, miR-215, miR-216, miR-146a, miR-204 and miR-886 is elevated in the kidney.<sup>9</sup> Urinary miRNAs represent a highly promising novel source of non-invasive biomarkers that are stabilised via argonaute 2 protein/exosome association and are rapidly and precisely detected by RT-qPCR.<sup>10</sup>

Reports have suggested a role for miRNAs in the pathology of DKD,<sup>11,12</sup> including previous work from this laboratory showing decreased miR-192 in biopsies from late-stage DKD patients with diminished renal function.<sup>13</sup> However, comparatively little is known about the abundance of urinary miRNAs in DKD patients.

We hypothesised that alterations in urinary miRNA profiles would be associated with DKD. We identified candidate DKD biomarkers by comparing miRNA profiles in urine samples from a patient discovery cohort with those from unaffected controls. Selected candidates were then measured in a larger, independent cohort. Subsequently, laser capture microdissection of renal biopsies and *in vitro* cell culture were used to investigate the sources of our candidate urinary miRNA DKD biomarkers with respect to nephron domain and cell type.

## Materials and Methods

### Study Participants

DKD was defined in accordance with the National Kidney Foundation Kidney Disease Outcomes Quality Initiative (NKF KDOQI) Clinical Practice Guidelines and Clinical Practice Recommendations for Diabetes and Chronic Kidney Disease (CKD).<sup>14</sup> Accordingly, CKD should be attributable to diabetes in the presence of macroalbuminuria (in the absence of urinary infection), or in the presence of microalbuminuria with concomitant diabetic retinopathy, or in type 1 diabetes of at least 10 years duration.<sup>14</sup> The initial profiling study cohort of 20 DKD patients and 20 healthy controls was obtained from the Wales Kidney Research Tissue Bank, University Hospital of Wales, Cardiff. The DKD group was predominantly male (85%), mean age 72 years (SD +/- 8.7). DKD patients were CKD stage 3-5 (pre-dialysis), with mean eGFR of 29 ml/min/1.73m<sup>2</sup> (SD +/- 8.5) and a mean urinary Albumin:Creatinine ratio (ACR) of 13.5 mg/mmol (SD +/- 14.5). The control group (n = 20) in the profiling cohort were 50% male, mean age 47 years (SD +/- 11.0) with no microalbuminuria (ACR<3 mg/mmol). For further details on ACR categories see Table 1.

The confirmation cohort was drawn from two secondary care facilities: the Wales Kidney Research Tissue Bank (as above) and the Renal Impairment In Secondary Care (RIISC) study, University Hospital of Birmingham, UK.<sup>15</sup> 89 patients with DKD, including 3 patients with type 1 diabetes, and 41 healthy controls were recruited across the two sites. An additional control group of 62 diabetics without DKD were recruited from Cardiff, including 17 patients with type 1 diabetes. Ethical approval

was granted by the Wales Kidney Research Tissue Bank Governance Committee and the South Birmingham Local Research Ethics Committee, respectively.

Patient demographics and clinical parameters are shown in Table 1. All patients were recruited from specialist nephrology and diabetes care services at the two sites during the period spanning autumn 2010 to autumn 2013. DKD patients from the RIISC study cohort were predominantly advanced nephropaths as per RIISC protocol inclusion criteria: briefly, patients with CKD stages 4-5 (pre-dialysis), or CKD stage 3 and accelerated progression and/or proteinuria as defined by the UK National Institute for Health and Care Excellence 2008 CKD guideline for secondary care review. The diabetic patient control group all had a diagnosis of diabetes by standard American Diabetes Association criteria,<sup>16</sup> but without evidence of DKD (i.e. not fulfilling the KDOQI criteria).

At initial clinic visit, renal function was recorded using estimated glomerular filtration rate (eGFR), calculated using the modification of diet in renal disease (MDRD) equation<sup>17</sup>. Urine samples were aliquoted for albumin:creatinine ratio (ACR) assessment and for RNA extraction (see below). ACR cut-offs for disease severity were defined as per Kidney Disease: Improving Global Outcomes (KDIGO) 2012 guidelines.<sup>18</sup>

#### **Urine Collection, RNA Isolation and RT-qPCR analysis**

Urine samples were collected and RNA extraction from 350 µl of urine, generation of cDNA from equal volumes of RNA extracts and RT-qPCR were then carried out as



described in detail elsewhere.<sup>10</sup> TaqMan assays (Thermo Fisher Scientific, Paisley, UK) used in this study were: hsa-miR-29b-3p (ID 000413); hsa-miR-126-3p (ID 002228); hsa-miR-155-5p (ID 002623); hsa-miR-191-5p (ID 002299). Relative quantities were calculated using the  $2^{-\Delta\Delta Ct}$  method, and miRNA expression was normalized to hsa-miR-191-5p.<sup>10</sup>

#### **MiRNA profiling by TaqManArray Human MicroRNA Cards**

Urinary miRNAs were reverse transcribed using the Megaplex Primer Pools (Human Pools A v2.1 and B v3.0, Thermo Fisher Scientific) with a predefined pool of 381 reverse transcription (RT) primers for each Megaplex Primer Pool. A fixed volume of 3 µl of RNA solution was used as input in each RT reaction, and RT reactions were performed according to the manufacturer's recommendations. RT reaction products were amplified using Megaplex PreAmp Primers (Primers A v2.1 and B v3.0, Thermo Fisher Scientific), the samples were then diluted to a final volume of 100 µl and control subject and DKD patient products were pooled as follows.

To exclude the possibility that gender, age and eGFR status had extreme effects on miRNA expression profiles, the following pooling strategy was followed. Control pool (CP)1: urine samples from 5 females of average age 44.8 years; CP2: 5 females, 57.6; CP3: 5 males, 35.2; CP4, 5 males, 53.2. Patient Pool (PP)1: urine samples from 5 CKD3 patients with an eGFR between 43.3 and 36 mL/min per 1.73m<sup>2</sup>; PP2: 5 stage 3 patients, 35 - 31; PP3: 5 stage 4/5 patients, 27.3 - 23; PP4: 5 stage 4/5 patients, 22 - 12.9.

TaqManArray Human MicroRNA Cards A v2.1 and B v3.0 (Thermo Fisher Scientific) were used to quantify 754 human miRNAs. Each array included 377 test miRNAs, 3 endogenous controls and a negative control. Quantitative (q)PCR was carried out on an Applied Biosystems 7900HT thermo cycler (Thermo Fisher Scientific) using the manufacturer's recommended program.

### **Laser Capture Microdissection (LCM) from Renal Biopsy Samples**

Glomeruli, proximal tubular and distal tubular profiles were microdissected from 6- $\mu$ m sections obtained from five FFPE archived renal biopsies from unaffected people using the Arcturus Pixcell Ile infrared laser enabled LCM system (Thermo Fisher Scientific).

### **Cell Culture**

Human conditionally immortalised glomerular endothelial cell (GEnC) and human podocyte (ATC) cell lines were propagated at 33°C as described previously.<sup>19,20</sup> After 5 (GEnC) and 14 (ATC) days, cells were transferred to 37°C incubation to inactivate the SV40 T antigen and permit differentiation, prior to experimental use. Where stated, GEnCs were growth arrested for 24 h and then treated with TNF- $\alpha$  (10 ng/mL) or TGF- $\beta$ 1 (1 ng/mL) at either normoglycaemic (5 mM) or hyperglycaemic (25 mM) D-glucose concentrations for 24 h. Proximal tubular epithelial cell (PTC) line HK-2<sup>21</sup> and fibroblast<sup>22</sup> cultures were maintained as described elsewhere. Cells and culture medium obtained from each well were used for RNA extraction as described above.

## 178 **Statistical analysis**

179 MiRNA profiling data were analysed using Thermo Fisher Scientific's DataAssist  
180 Software (version 3.01), NormFinder Software ([http://moma.dk/normfinder-](http://moma.dk/normfinder-software)  
181 [software](http://moma.dk/normfinder-software); last access 21/02/18) and GraphPad Prism 6 (version 6.0d). Pearson  
182 Correlation Coefficients was used to detect clusters of similarity in miRNA threshold  
183 cycle values between each pool group in patients, and between each pool group in  
184 controls. To identify a suitable reference gene for the normalization of miRNA  
185 expression in this study, the NormFinder algorithm was applied to the expression  
186 data obtained from the Human TaqMan miRNA Arrays. Analysis comparing miRNA  
187 levels between subjects with DKD and controls was carried out using GraphPad Prism  
188 version 6 version 6.0d. Values for p below 0.05 were considered statistically  
189 significant. MiRNA profiling data sets can be found in Gene Expression Omnibus  
190 (<https://www.ncbi.nlm.nih.gov/geo>; accession number GSE114477).

191

## Results

### Altered urinary miRNA detection in DKD patients

To select candidate miRNAs that may act as DKD biomarkers, we first compared data from unbiased expression profiling of 754 miRNAs in urine samples from 20 DKD patients and 20 unaffected controls. Analyses were performed on 4 patient and 4 control pools, each composed of urine samples from 5 individuals as recommended by Zhang and colleagues.<sup>23</sup> Samples were pooled prior to profiling to minimize the contribution of subject to subject variation and to make substantive features easier to find, and thereby identify biomarkers common across individuals.<sup>24</sup> Previous analysis suggested that 40 individuals might optimally be pooled across 8 arrays,<sup>23</sup> which was our chosen pooling approach.

In Figure 1A the 12 data points in the upper right quadrant of the plot represent those miRNAs for which statistically significant fold-change increases were detected in patient urine compared to control samples, the 35 points in the upper left quadrant the corresponding downregulated miRNAs. The fold-change data for these 47 miRNAs are summarised in Figure 1B, and the 8 miRNAs exhibiting >5-fold change were subsequently selected as potential candidate biomarkers for further analysis.

Specific RT-qPCR assays were then used to analyse these miRNAs in each component urine sample pooled for profiling analysis. Statistically significant differences in miRNA detection between DKD patient and control urine samples were replicated for miR-126 (4.3-fold increase;  $p = 0.0087$ ), miR-155 (22.9-fold;  $p = 0.0024$ ) and miR-29b (4.9-fold;  $p = 0.0002$ ) (Figure 1, C-E).

## **Elevated urinary miR-126, miR-155 and miR-29b detection in an independent DKD patient cohort**

To test the above findings, miR-126, miR-155 and miR-29b were quantified in samples from an independent cohort of patients with established DKD from the Renal Impairment in Secondary Care Study (RIISC).<sup>15</sup> Samples from 89 patients meeting the criteria established in the UK National Institute for Health and Care Excellence 2008 criteria were available. An additional cohort of 62 patients with diabetes mellitus but without proteinuria or other evidence of DKD were included, as were samples from 41 people without evidence of diabetes or DKD (Table 1). We included diabetes patients without DKD as a third group in this analysis to identify DKD-specific miRNA detection changes and not purely hyperglycaemia-driven effects from our profiling comparison of DKD patients with control individuals.

Significant differences were again seen between DKD patients and controls for miR-126 (2.8-fold increase;  $p < 0.0001$ ; Figure 2A), miR-155 (1.8-fold;  $p < 0.001$ ; Figure 2B) and miR-29b (4.6-fold;  $p = 0.024$ ; Figure 2C). Comparison of DKD patients with diabetic patients without DKD was statistically significant for miR-126 (3.1-fold increase;  $p < 0.0001$ ) and miR-155 (1.6-fold;  $p = 0.024$ ) with a trend to increased miR-29b (4.1-fold;  $p = 0.121$ ) (Figure 2A-C).

RT-qPCR data for all 3 miRNAs were used to compare DKD patients and diabetic patients without DKD in the combined receiver operating characteristic (ROC) curve analysis shown in Figure 2D, giving an area under the curve (AUC) of 0.80. To analyse the contributions of each miRNA to the above ROC curve, individual specificity and likelihood ratios were calculated for relative expression (RQ) values

equivalent to a sensitivity of 80%.<sup>25,26</sup> Data displayed in Table 2 illustrate the magnitude of corresponding specificity values was miR-126 > miR-155 > miR-29b, and that combined miRNA data resulted in a  $\geq 6.5\%$  increase in specificity and likelihood ratio compared with individual miRNAs. These RQ data were then used as consecutive threshold values to discriminate between DKD and diabetic patients without DKD (D in Table 3) from the independent cohort. The discriminatory order was miR-29b (DKD/D = 5.62) > miR-126 (3.48) > miR-155 (2.23), and RQ values exceeding all 3 thresholds were obtained for 48.0% of DKD patients compared with 3.6% of diabetic patients without DKD (Table 3).

#### **Laser capture microdissection shows increased glomerular abundance of miR-126 and miR-29b that is replicated in GEnC culture**

Previous reports have linked changes in miRNA expression to DKD pathology, but have focused on whole tissue studies. For example, we showed association of decreased miR-192 expression with disease progression in DKD biopsies by *in situ* hybridisation.<sup>13</sup>

In the present study we used laser capture microdissection (LCM) to isolate glomeruli, proximal and distal tubules (Figure 3A) from histologically normal formalin-fixed, paraffin-embedded (FFPE) renal biopsy samples, and analysed miR-126, miR-155 and miR-29b expression by RT-qPCR. In Figure 3B, a typical CD10-stained FFPE biopsy section is seen before and after LCM to isolate glomeruli, proximal and distal renal tubules. MiR-126, miR-155 and miR-29b were detected in extracts from all three nephron regions (Figure 3, C-E). Increased glomerular

abundances were observed for miR-126 (Figure 3C) and miR-29b (Figure 3E), while miR-155 was most abundant in the distal tubule (Figure 3D).

Conclusions regarding nephron region-specific miRNA expression from the above analyses are inherently limited, however, since tissue extracts are subject to trace contamination by cells from other nephron domains. Therefore, cellular miRNA localisation within each nephron region was subsequently investigated by RT-qPCR analysis of podocyte and endothelial cell (GEnC) cultures from the glomerulus, renal proximal tubular epithelial cells (PTC) and fibroblasts. Detection of miR-126 was significantly higher in GEnCs compared with other cell types (Figure 3F). Most miR-155 was detected in PTCs and least in GEnCs (Figure 3G), while miR-29b was most abundant in GEnCs (Figure 3H).

#### **GEnC release of miR-126 and miR-29b in an *in vitro* model of hyperglycaemia is driven by TNF- $\alpha$ and TGF- $\beta$ 1, respectively**

The above data localized the majority of miR-126 and miR-29b expression to the GEnC. We next sought stimuli by which miRNAs are released into the glomerular ultrafiltrate, and hence the urine. Data from animal models of diabetes show increased glomerular and PTC TNF- $\alpha$  expression, and renoprotective effects of TGF- $\beta$  inhibitors have also been reported.<sup>27,28</sup> GEnC expression of our candidate miRNAs was thus analysed *in vitro* in response to TNF- $\alpha$  and TGF- $\beta$ 1 in normoglycaemia and hyperglycaemia (Figure 4, A-F).

The presence of TNF- $\alpha$  led to significantly increased miR-126 detection in GEnC conditioned medium at 5 mM and 25 mM D-glucose (Figure 4B), a pattern also seen for miR-29b following TGF- $\beta$ 1 addition (Figure 4D). These cytokines did not

increase GEnC expression of miR-126 (Figure 4A), or miR-29b (Figure 4C), a pattern consistent with increased release, but not expression, of miRNAs.

No significant changes in miR-155 were detected in response to elevated D-glucose with either cytokine, and data for TNF- $\alpha$  are shown (Figure 4, E and F). Similarly, changes in miR-126 following TGF- $\beta$ 1 addition, and for miR-29b in the presence of TNF- $\alpha$ , were not observed (data not shown). Elevated D-glucose alone did not change miRNA expression in GEnCs or conditioned medium (Figure 4, A-F).



## Discussion

Diabetic kidney disease (DKD) is the leading cause of kidney failure requiring renal replacement therapy worldwide, but effective methods to identify and halt progression of disease-specific pathophysiological changes remain elusive. Current effective interventions such as control of blood glucose and blood pressure are challenging to achieve, costly and time intensive. Existing tests track DKD from diabetic diagnosis to kidney failure, but do not allow accurate prognosis for the individual patient. In addition, the absence of treatment response biomarkers hinders development of emerging DKD therapies. There is thus an unmet need for additional DKD biomarkers to target intervention and follow response to therapy.

In this study we set out to identify urinary miRNA DKD biomarkers. Increased detection of miR-126, miR-155 and miR-29b was observed in the urine of DKD patients in comparison with both unaffected individuals and diabetic patients without DKD. MiRNA localization and release studies further suggested specific release of miR-126 and miR-29b from GEnCs. This raised the possibility that urinary miRNA quantification might provide data on ongoing pathological processes, and so aid patient stratification and measurement of response to therapy.

Urinary miRNA biomarkers have several potential significant advantages over circulating miRNAs for adoption into existing treatment pathways alongside current biomarkers, including speed and cost of non-invasive sample access.<sup>29</sup> However, few urinary miRNA DKD biomarker data have so far been reported. Previous studies have focused on circulating miRNAs, and have generated conflicting data with respect to association of miR-126 with diabetes mellitus and/or DKD. A recent cross-sectional analysis of type 2 diabetes mellitus patients found a negative association with

plasma miR-126,<sup>30</sup> and similar findings have been reported for type 1 diabetes mellitus and all complications.<sup>31</sup> By contrast, miR-126 detection did not change in whole blood from type 2 diabetes mellitus patients and control subjects, but decreased in DKD patient samples.<sup>32</sup> Furthermore, no change in plasma miR-126 was observed in a study of paediatric type 1 diabetic patients.<sup>33</sup> These analyses provide inconsistent data for the biomarker utility of circulating miR-126, in contrast to the significant and reproducible increases we detected in miR-126, miR-155 and miR-29b in DKD patient urine in the present study.

The DKD-specific alterations in urinary miRNA profiles detected in this study may have functional significance. Our *in vitro* analyses localized miR-126 and miR-29b principally to the GEnC, with miR-155 expression distributed evenly across the nephron. Glomerular endothelial localization of miR-126 may reflect the role of this transcript in vascular regulation. Targeted mouse miR-126 deletion resulted in vascular abnormalities by removing inhibition of sprouty-related EVH1 domain-containing protein 1 expression, thereby enhancing vascular endothelial growth factor (VEGF) function.<sup>34</sup> A role in DKD pathology for VEGFA signalling between GEnCs and podocytes has been proposed.<sup>35</sup> In addition, miR-126 repression of vascular cell adhesion molecule 1 expression in human umbilical vein endothelial cells regulates their response to pro-inflammatory adhesion molecules.<sup>36</sup> MiR-126 has also been implicated in the heterogenic inflammatory response of renal microvascular endothelial cells.<sup>37</sup>

Increased expression of miR-155 has been observed in DKD patient renal biopsies, in close correlation with increased serum creatinine.<sup>38</sup> Furthermore, miR-155 deficiency attenuated renal damage and IL-17 expression was downregulated in

streptozotocin-induced DKD mice.<sup>39</sup> Together with miR-126, miR-155 has been implicated in multiple forms of vascular remodelling and associated with cardiovascular disease.<sup>40</sup>

Decreased miR-29b has been reported in early and advanced animal models of diabetic renal fibrosis.<sup>41</sup> Chen and colleagues found that loss of renal miR-29b in db/db mice led to increased albuminuria, TGF- $\beta$ -mediated fibrosis and immune injury, while restored miR-29b expression inhibited renal injury.<sup>42</sup> Indeed, while we have focused on upregulated miRNAs in this study, we acknowledge the potential importance of miRNA downregulations that we detected.

In the present study we localized miR-29b to the glomerular endothelium. Reduction of collagen and laminin synthesis has been reported following forced miR-29b expression in human corneal endothelial cells.<sup>43</sup> In apoE knockout mice, miR-29b induced aortic endothelial permeability in response to a high fat diet, and brought about aortic apoptosis by direct targeting of melatonin receptor mt1.<sup>44</sup> In addition, upregulated miR-29b expression has been observed in human umbilical vein endothelial cells exposed to hyperglycaemia.<sup>45</sup>

The cytokine-driven release from GEnCs observed for miR-126 (TNF- $\alpha$ ) and miR-29b (TGF- $\beta$ 1) reported here suggests that these cells may be the principal source of elevated urinary miR-126 and miR-29b detected in DKD. We speculate that this constitutes evidence for disease-related signalling down the nephron that will be interesting to test in future studies. Indeed, we have demonstrated association of urinary miRNAs with exosomes<sup>10</sup> and exosomal transport, which might facilitate passage of miRNAs through the nephron, has been reported for all three candidate biomarker miRNAs.

365 Exosome-mediated release of miR-126 from CD34<sup>+</sup> peripheral blood  
366 mononuclear cells is proangiogenic, and decreased miR-126 was detected in  
367 elevated glucose cell culture and diabetic patients.<sup>46</sup> MiR-155 is depleted in urinary  
368 exosomes from microalbuminuric type 1 diabetes mellitus patients.<sup>47</sup> Endogenous  
369 miR-29b, spontaneously released from beta-cells within exosomes, stimulates TNF-  
370  $\alpha$  secretion from spleen cells isolated from diabetes-prone NOD mice *in vitro*.<sup>48</sup>

371 In summary, we have used unbiased profiling approaches to identify a urinary  
372 miRNA signature associated with DKD, and have subsequently confirmed increased  
373 miR-126, miR-155 and miR-29b in an independent patient cohort. MiR-126 and miR-  
374 29b were identified as enriched in GEnCs, and released from these cells in response  
375 to DKD-related cytokines. Urinary miR-126, miR-155 and miR-29b are therefore  
376 promising DKD biomarkers, and the potential pathological significance of miR-126  
377 and miR-29b release from GEnCs merits further evaluation.

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## Figure legends

**Figure 1** Urinary miRNA detection in urine samples from DKD patients and control subjects. **A:** Volcano plot showing the detection profile of the 377 urinary miRNAs in TLDA Card A in DKD patients (n = 20; four pools of five patients) and controls (n = 20; four pools of five controls). The dotted horizontal line represents a p value boundary of 0.05. **B:** Fold change of miRNA detection between DKD patients and controls. DataAssist Software (Thermo Fisher Scientific) was used to perform relative quantification for sample comparison, to perform t-test sample group comparisons, and to produce the graphic output shown. **(C-E)** RT-qPCR analysis shows significant differences in detection of **(C)** miR-126, **(D)** miR-155 and **(E)** miR-29b between patients and control urine in the component urine samples pooled for profiling analyses **(A and B)**. DKD patients versus controls for **C:** miR-126, **D:** miR-155, **E:** miR-29b (n = 20 for each group). Analysis was carried out by unpaired 2-tailed t-test with Welch's correction. Profiling data analysis using the NormFinder algorithm identified miR-191 as optimal for normalisation of our RT-qPCR data. Data were normalized to endogenous control miR-191 and are presented as mean +/- SEM. \*\* $P < 0.01$ , \*\*\* $P < 0.005$  and \*\*\*\* $P < 0.0005$ .

**Figure 2** RT-qPCR detection of selected miRNAs in patients and control subjects. Relative expression was significantly different in 89 DKD patients compared with 62 diabetic patients without DKD and 41 controls for **(A)** miR-126 and **(B)** miR-155, and significantly different in DKD patients compared with controls for **(C)** miR-29b. **A:** DKD patients versus diabetic patients without DKD and controls; **B:** DKD patients and diabetic patients without DKD; DKD patients versus controls; **C:** DKD patients versus

controls (n = 89 DKD patients, 62 diabetic patients without DKD, 41 controls). Analysis was carried out by unpaired 1-tailed t-test with Welch's correction. Data were normalized to endogenous control miR-191 and are presented as mean +/- SEM. **(D)** Combined receiver operating characteristic curve analysis for miR-126, miR-155 and miR-29b, area under the curve (AUC) = 0.80. Data were generated using the pROC package in R-3.2.3. \* $P < 0.05$ , \*\*\*\* $P < 0.001$  and \*\*\*\*\* $P < 0.0001$ .

**Figure 3** Localization of miRNA expression by laser capture microdissection (LCM) and cell culture. **A:** Key functional nephron domains include the glomerulus (G), the proximal tubule (PT) and the distal tubule (DT). **B:** A CD10-stained FFPE renal biopsy sample before and after excision of glomeruli by LCM. Bars = 100  $\mu$ m. **(C-E)** Relative expression of miR-126, miR-155 and miR-29b, respectively, in LCM-isolated Gs, PTs and DTs from 5 renal biopsies of healthy individuals. **C:** G versus PT; G versus DT (n = 5 biopsies). **(F-H)** Relative expression of miR-126, miR-155 and miR-29b, respectively, in *in vitro* cultured HK-2 renal proximal tubular epithelial cells (PTCs), fibroblasts, podocytes and conditionally immortalized glomerular endothelial cells (GEnCs). **F:** GEnCs versus fibroblasts; GEnCs versus PTCs and podocytes; **G:** PTC versus GEnCs; **H:** GEnCs versus podocytes (n = 4). Analysis was carried out by one-way ANOVA analysis with Tukey's multiple comparison test. Data were normalized to endogenous control miR-191 and are presented as mean +/- SEM. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\*\* $P < 0.001$ .

**Figure 4** MiRNA expression in GenCs and GenC conditioned medium in response to hyperglycaemia and DKD-related cytokines. Following 24 h culture in 5 mM or 25 mM D-glucose, relative expression in GEnCs and GEnC conditioned medium, respectively, of **(A and B)** miR-126 in response to 10 ng/ml TNF- $\alpha$ , **(C and D)** miR-29b in response to 1 ng/ml TGF- $\beta$ 1 and **(E and F)** miR-155 in response to 10 ng/ml TNF- $\alpha$ , and in untreated cells. **B:** 5 mM D-glucose versus 5 mM D-glucose plus TNF- $\alpha$ , and 25 mM D-glucose versus 25 mM D-glucose plus TNF-  $\alpha$ ; **C:** 5 mM D-glucose versus 5 mM D-glucose plus TGF- $\beta$ 1, and 25 mM D-glucose versus 25 mM D-glucose plus TGF- $\beta$ 1; **D:** 5 mM D-glucose versus 5 mM D-glucose plus TGF- $\beta$ 1; 25 mM D-glucose versus 25 mM D-glucose plus TGF- $\beta$ 1 (n = 4). Analysis was carried out by one-way ANOVA analysis with Tukey's multiple comparison test. Data were normalized to endogenous control miR-191 and are presented as mean  $\pm$  SEM. \* $P$  < 0.05 and \*\* $P$  < 0.01.

**Table 1** Demographic and clinical parameters of patients recruited from 2 centres:  
Wales Kidney Research Tissue Bank, Cardiff (University Hospital Wales) and  
Birmingham (University Hospital Birmingham, Renal Impairment in Secondary care  
(RIISC) study cohort) (n = 151)

Feature	Patients (n=151)		Controls (n=41)
	Diabetic (n=62)	DKD (n=89)	
Male n (%)	37 (58)	55 (62)	18 (44)
Non-Caucasian n (%)	13 (21)	33 (37)	
Mean Age (years, SD)	52 +/- 16.1	62 +/- 13.6	55 +/- 15.4
eGFR ml/min/1.73m <sup>2</sup>			
Mean (SD)	78 +/-16.3	30 +/- 20.9	
Median (IQR)	84 (72-90)	22 (17-38)	
CKD stage n(%)			
No CKD/CKD G1 (eGFR ≥ 90)	23 (37)	2 (2)	
CKD G2 (eGFR = 60-89)	32 (52)	10 (11)	
CKD G3 (eGFR = 30-59)	5 (8)	17 (19)	
CKD G4 (eGFR = 15-29)	2 (3)	45 (51)	
CKD G5 (eGFR <15)	0	15 (17)	
ACR* mg/mmol n(%)			
A1-Normal-high normal (ACR<3)	54 (87.1)	15 (16.9)	
A2-Moderately increased (ACR 3-30)	8 (12.9)	25 (28.1)	
A3-Severely increased (ACR>30)	0 (0)	49 (55.0)	

\*Albumin:Creatinine ratio (ACR) group cut-offs and nomenclature derived from  
KDIGO 2012 recommendations.



**Table 2** Specificity values, likelihood ratios and RQ thresholds for miR-126, miR-155, miR-29b and all three miRNAs above an 80% ROC curve sensitivity threshold

	Sensitivity (%)	Specificity (%)	Likelihood Ratio	RQ Threshold
3 miRNAs	80.21	63.64	2.206	> 1.148
miR-126	80.41	57.14	1.876	> 0.6762
miR-155	80.61	52.00	1.679	> 0.9110
miR-29b	80.61	40.00	1.344	> 0.8058

**Table 3** DKD and diabetic patients without DKD (D) patient numbers and percentages above an 80% ROC curve sensitivity threshold for miR-126, miR-155, miR-29b and all three miRNAs

	Patients above 80% sensitivity threshold				Total
	miR-126	miR-155	miR-29b	3 miRNAs	
D	23	30	13	2	55
DKD	80	67	73	47	98

	Percentage of patients above 80% sensitivity threshold			
	miR-126	miR-155	miR-29b	3 miRNAs
D	41.8	54.6	23.6	3.6
DKD	81.6	68.4	74.5	48.0

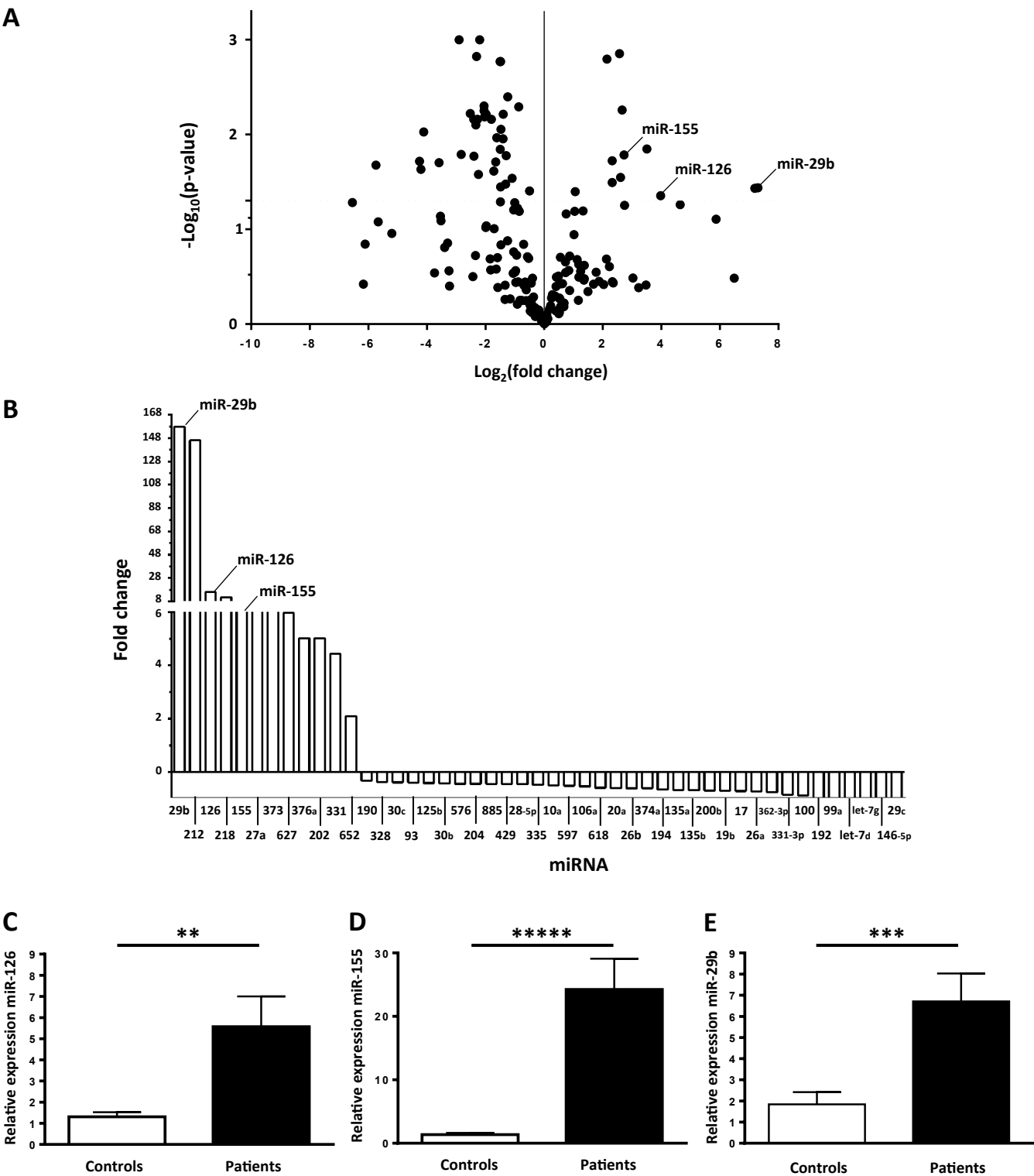
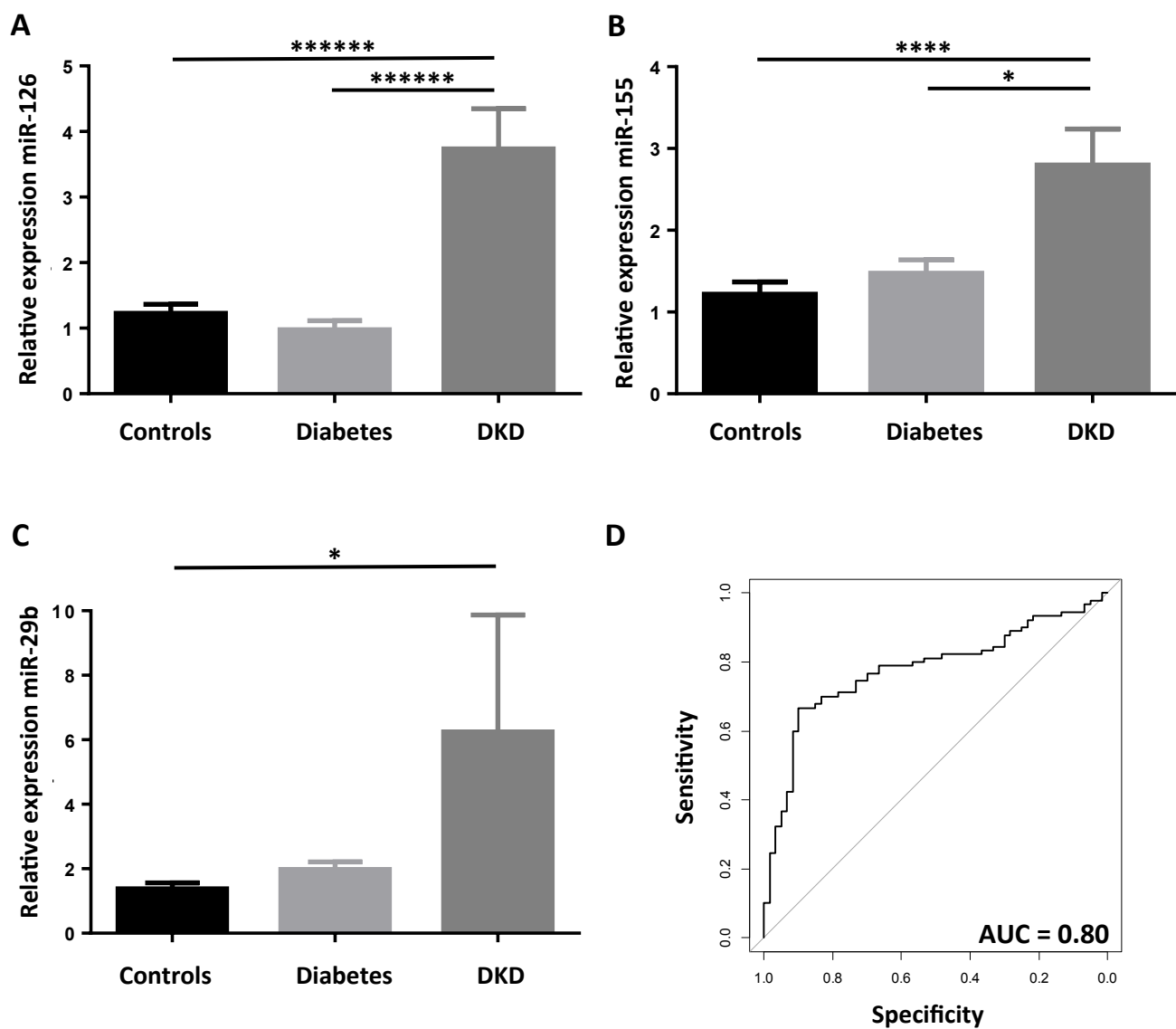
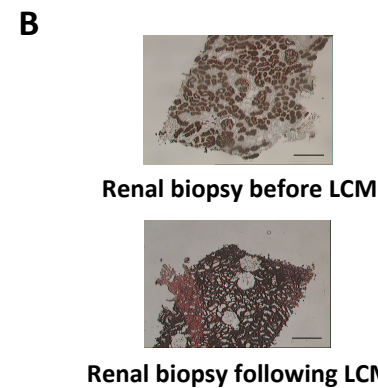
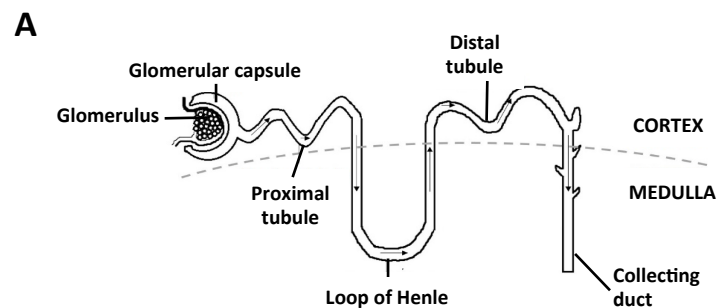


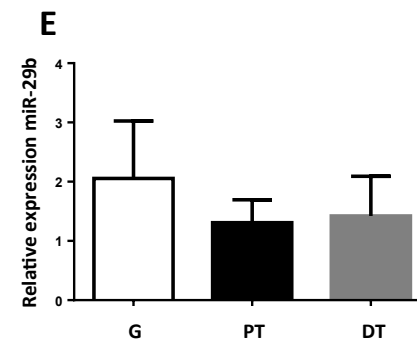
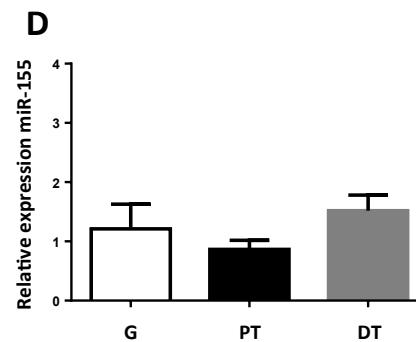
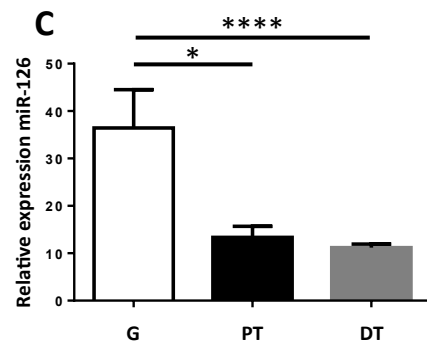
Figure 1



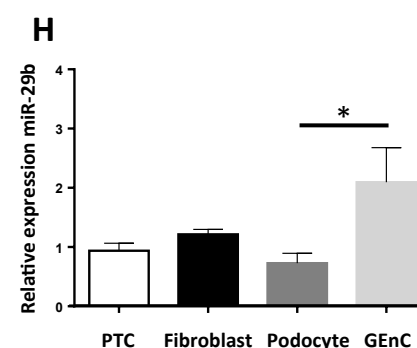
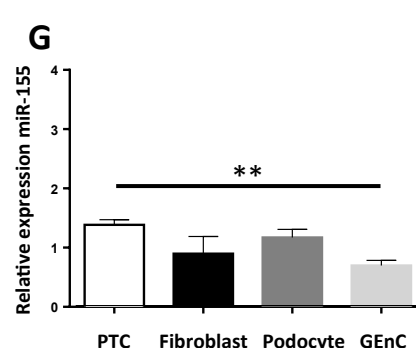
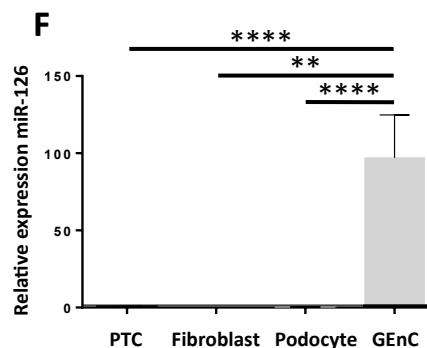
**Figure 2**



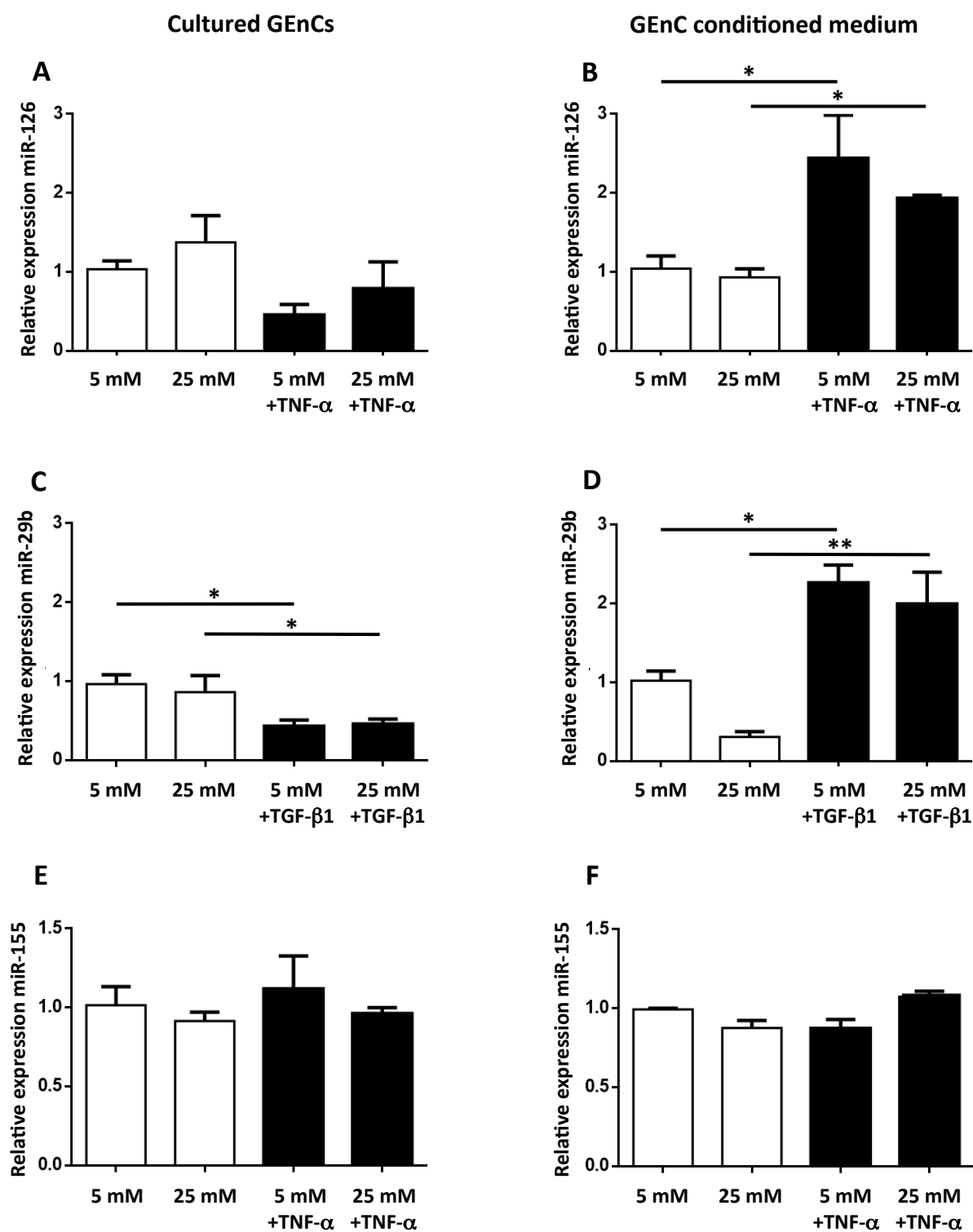
LCM-dissected  
nephron domains



Cell cultures



**Figure 3**



**Figure 4**